

# SEQUENCE LISTING

<110> Dale Umetsu  
Rosemarie DeKruyff  
Jennifer McIntire  
Gordon Freeman

<120> T CELL REGULATORY GENES ASSOCIATED WITH  
IMMUNE DISEASE

<130> STAN-235CIP

<150> 60/302,344

<151> 2001-06-29

<150> 10/188,012

<151> 2002-07-01

<160> 40

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 305

<212> PRT

<213> M. musculus

<220>

<221> VARIANT

<222> (1)...(305)

<223> TIM-1 BALB/c allele

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Val	Thr	Leu	Pro	Cys	Thr	Tyr	Ser	Thr	Tyr	Arg	Gly	Ile	Thr	Thr	Thr
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Cys	Trp	Gly	Arg	Gly	Gln	Cys	Pro	Ser	Ser	Ala	Cys	Gln	Asn	Thr	Leu
	50					55				60					
Ile	Trp	Thr	Asn	Gly	His	Arg	Val	Thr	Tyr	Gln	Lys	Ser	Ser	Arg	Tyr
65					70				75					80	
Asn	Leu	Lys	Gly	His	Ile	Ser	Glu	Gly	Asp	Val	Ser	Leu	Thr	Ile	Glu
				85					90					95	
Asn	Ser	Val	Glu	Ser	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Arg	Val	Glu	Ile
			100					105					110		
Pro	Gly	Trp	Phe	Asn	Asp	Gln	Lys	Val	Thr	Phe	Ser	Leu	Gln	Val	Lys
		115					120					125			
Pro	Glu	Ile	Pro	Thr	Arg	Pro	Pro	Thr	Arg	Pro	Thr	Thr	Thr	Arg	Pro
	130					135					140				
Thr	Ala	Thr	Gly	Arg	Pro	Thr	Thr	Ile	Ser	Thr	Arg	Ser	Thr	His	Val
145					150					155					160
Pro	Thr	Ser	Ile	Arg	Val	Ser	Thr	Ser	Thr	Pro	Pro	Thr	Ser	Thr	His
				165					170					175	
Thr	Trp	Thr	His	Lys	Pro	Glu	Pro	Thr	Thr	Phe	Cys	Pro	His	Glu	Thr
			180					185					190		
Thr	Ala	Glu	Val	Thr	Gly	Ile	Pro	Ser	His	Thr	Pro	Thr	Asp	Trp	Asn
		195					200						205		

Gly Thr Val Thr Ser Ser Gly Asp Thr Trp Ser Asn His Thr Glu Ala  
 210 215 220  
 Ile Pro Pro Gly Lys Pro Gln Lys Asn Pro Thr Lys Gly Phe Tyr Val  
 225 230 235 240  
 Gly Ile Cys Ile Ala Ala Leu Leu Leu Leu Leu Val Ser Thr Val  
 245 250 255  
 Ala Ile Thr Arg Tyr Ile Leu Met Lys Arg Lys Ser Ala Ser Leu Ser  
 260 265 270  
 Val Val Ala Phe Arg Val Ser Lys Ile Glu Ala Leu Gln Asn Ala Ala  
 275 280 285  
 Val Val His Ser Arg Ala Glu Asp Asn Ile Tyr Ile Val Glu Asp Arg  
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 Pro  
 305

<210> 2  
 <211> 918  
 <212> DNA  
 <213> Mus musculus

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 acatatcggtg gaatcacaaac gacatggttg ggccgagggc aatgcccac ttctgcttgt 180  
 caaaatacac ttatttggac caatggacat cgtgtcacct atcagaagag cagtcggtac 240  
 aacttaaagg ggcataatttc agaaggagat gtgtccttga cgatagagaa ctctgttgag 300  
 agtgacagtg gtctgtattg ttgtcgagtg gagattcctg gatggtttaa tgatcagaaa 360  
 gtgacctttt cattgcaagt taaaccagag attcccacac gtcctccaac aagaccaca 420  
 actacaaggc ccacagctac aggaagaccc acgactattt caacaagatc cacacatgta 480  
 ccaacatcaa tcagagtctc tacctccact cctccaacat ctacacacac atggactcac 540  
 aaaccagaac ccactacatt ttgtcccat gagacaacag ctgaggtgac aggaatccca 600  
 tcccatactc ctacagactg gaatggcact gtgacatcct caggagatac ctggagtaat 660  
 cacactgaag caatccctcc agggaagccg cagaaaaacc ctactaaggg cttctatgtt 720  
 ggcacatgca tcgcagccct gctgctactg ctcttgtga gcaccgtggc tatcaccagg 780  
 tacatactta tgaaaaggaa gtcagcatct ctaagcgtgg ttgccttcg tgtctctaag 840  
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<210> 3  
 <211> 282  
 <212> PRT  
 <213> Mus musculus

<220>  
 <221> VARIANT  
 <222> (1)...(282)  
 <223> TIM-1, C.D2 ES-HBA and DBA/2J allele

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 Gly Ala Val Asp Ser Tyr Val Glu Val Lys Gly Val Val Gly His Pro  
 20 25 30  
 Val Thr Leu Pro Cys Thr Tyr Ser Thr Tyr Arg Gly Ile Thr Thr Thr  
 35 40 45  
 Cys Trp Gly Arg Gly Gln Cys Pro Ser Ser Ala Cys Gln Asn Thr Leu  
 50 55 60  
 Ile Trp Thr Asn Gly His Arg Val Thr Tyr Gln Lys Ser Ser Arg Tyr  
 65 70 75 80  
 Asn Leu Lys Gly His Ile Ser Glu Gly Asp Val Ser Leu Thr Ile Glu



1				5					10					15			
Gly	Ala	Val	Glu	Ser	His	Thr	Ala	Val	Gln	Gly	Leu	Ala	Gly	His	Pro		
			20					25					30				
Val	Thr	Leu	Pro	Cys	Ile	Tyr	Ser	Thr	His	Leu	Gly	Gly	Ile	Val	Pro		
		35					40					45					
Met	Cys	Trp	Gly	Leu	Gly	Glu	Cys	Arg	His	Ser	Tyr	Cys	Ile	Arg	Ser		
	50					55					60						
Leu	Ile	Trp	Thr	Asn	Gly	Tyr	Thr	Val	Thr	His	Gln	Arg	Asn	Ser	Arg		
65					70					75					80		
Tyr	Gln	Leu	Lys	Gly	Asn	Ile	Ser	Glu	Gly	Asn	Val	Ser	Leu	Thr	Ile		
			85						90					95			
Glu	Asn	Thr	Val	Val	Gly	Asp	Gly	Gly	Pro	Tyr	Cys	Cys	Val	Val	Glu		
			100					105					110				
Ile	Pro	Gly	Ala	Phe	His	Phe	Val	Asp	Tyr	Met	Leu	Glu	Val	Lys	Pro		
		115					120					125					
Glu	Ile	Ser	Thr	Ser	Pro	Pro	Thr	Arg	Pro	Thr	Ala	Thr	Gly	Arg	Pro		
	130					135					140						
Thr	Thr	Ile	Ser	Thr	Arg	Ser	Thr	His	Val	Pro	Thr	Ser	Thr	Arg	Val		
145					150					155					160		
Ser	Thr	Ser	Thr	Ser	Pro	Thr	Pro	Ala	His	Thr	Glu	Thr	Tyr	Lys	Pro		
				165				170						175			
Glu	Ala	Thr	Thr	Phe	Tyr	Pro	Asp	Gln	Thr	Thr	Ala	Glu	Val	Thr	Glu		
			180					185					190				
Thr	Leu	Pro	Ser	Thr	Pro	Ala	Asp	Trp	His	Asn	Thr	Val	Thr	Ser	Ser		
		195					200					205					
Asp	Asp	Pro	Trp	Asp	Asp	Asn	Thr	Glu	Val	Ile	Pro	Pro	Gln	Lys	Pro		
	210					215					220						
Gln	Lys	Asn	Leu	Asn	Lys	Gly	Phe	Tyr	Val	Gly	Ile	Ser	Ile	Ala	Ala		
225					230					235					240		
Leu	Leu	Ile	Leu	Met	Leu	Leu	Ser	Thr	Met	Val	Ile	Thr	Arg	Tyr	Val		
				245					250					255			
Val	Met	Lys	Arg	Lys	Ser	Glu	Ser	Leu	Ser	Phe	Val	Ala	Phe	Pro	Ile		
			260					265					270				
Ser	Lys	Ile	Gly	Ala	Ser	Pro	Lys	Lys	Val	Val	Glu	Arg	Thr	Arg	Cys		
		275					280					285					
Glu	Asp	Gln	Val	Tyr	Ile	Ile	Glu	Asp	Thr	Pro	Tyr	Pro	Glu	Glu	Glu		
	290					295						300					
Ser																	
305																	

<210> 6  
 <211> 958  
 <212> DNA  
 <213> Mus musculus

<400> 6  
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 tcacctgtc acacttccat gtatttattc gacacacctt ggtggaatcg ttcctatgtg 180  
 ttggggccta ggggaatgcc gccattctta ttgtatacgg tcacttatct ggaccaatgg 240  
 atatacggtc acacatcaga ggaacagtcg ataccagcta aagggaata tttcagaagg 300  
 aaatgtgtcc ttgaccatag agaacactgt tgtgggtgat ggtggtcctt attgctgtgt 360  
 agtggagata cctggagcgt tccattttgt ggactatatg ttggaagtta aaccagaaat 420  
 ttccacgagt ccaccaacaa ggcccacagc tacaggaaga cccacaacta tttcaacaag 480  
 atccacacat gtaccaacat caaccagagt ctctacctct acttctccaa caccagcaca 540  
 cacagagacc tacaaccag aggccactac attttatcca gatcagacta cagctgaggt 600  
 gacagaaacc ttacctcta ctctgcaga ctggcataac actgtgacat cctcagatga 660  
 cccttgggat gataacactg aagtaatccc tccacagaag ccacagaaaa acctgaataa 720  
 gggcttctat gttggcatct ccattgcagc cctgctgata ttgatgcttc tgagcaccat 780  
 ggttatcacc aggtacgtgg ttatgaaaag gaagtcagaa tctctgagct ttgttgccct 840

ccctatctct aagattggag cttcccccaa aaaagtggtc gaacggacca gatgtgaaga 900  
ccaggtctac attattgaag acactcctta ccctgaagaa gattcctagt gcctctac 958

<210> 7  
<211> 305  
<212> PRT  
<213> Mus musculus

<220>  
<221> VARIANT  
<222> (1)...(305)  
<223> TIM-2, C.D2 ES-HBA and DBA/2J allele

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20 25 30  
Val Thr Leu Pro Cys Ile Tyr Ser Thr His Leu Gly Gly Ile Val Pro  
35 40 45  
Met Cys Trp Gly Leu Gly Glu Cys Arg His Ser Tyr Cys Ile Arg Ser  
50 55 60  
Leu Ile Trp Thr Asn Gly Tyr Thr Val Thr His Gln Arg Asn Ser Arg  
65 70 75 80  
Tyr Gln Leu Lys Gly Asn Ile Ser Glu Gly Asn Val Ser Leu Thr Ile  
85 90 95  
Glu Asn Thr Val Val Gly Asp Gly Gly Pro Tyr Cys Cys Val Val Glu  
100 105 110  
Ile Pro Gly Ala Phe His Phe Val Asp Tyr Met Leu Glu Val Lys Pro  
115 120 125  
Glu Ile Ser Thr Ser Pro Pro Thr Arg Pro Thr Ala Thr Gly Arg Pro  
130 135 140  
Thr Thr Ile Ser Thr Arg Ser Thr His Val Pro Thr Ser Thr Arg Val  
145 150 155 160  
Ser Thr Ser Thr Ser Pro Thr Pro Ala His Thr Glu Thr Tyr Lys Pro  
165 170 175  
Glu Ala Thr Thr Phe Tyr Pro Asp Gln Thr Thr Ala Glu Val Thr Glu  
180 185 190  
Thr Leu Pro Ser Thr Pro Ala Asp Trp His Asn Thr Val Thr Ser Ser  
195 200 205  
Asp Asp Pro Trp Asp Asp Asn Thr Glu Val Ile Pro Pro Gln Lys Pro  
210 215 220  
Gln Lys Asn Leu Asn Lys Gly Phe Tyr Val Gly Ile Ser Ile Ala Ala  
225 230 235 240  
Leu Leu Ile Leu Met Leu Leu Ser Thr Met Val Ile Thr Arg Tyr Val  
245 250 255  
Val Met Lys Arg Lys Ser Glu Ser Leu Ser Phe Val Ala Phe Pro Ile  
260 265 270  
Ser Lys Ile Gly Ala Ser Pro Lys Lys Val Val Glu Arg Thr Arg Cys  
275 280 285  
Glu Asp Gln Val Tyr Ile Ile Glu Asp Thr Pro Tyr Pro Glu Glu Glu  
290 295 300  
Ser  
305

<210> 8  
<211> 958  
<212> DNA  
<213> Mus musculus

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<400> 8
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tcacctgtc acacttccat gtattttattc gacacacctt ggtggaatcg ttcctatgtg 180
ttggggccta ggggaatgcc gccattctta ttgtatacgg tcacttatct ggaccaatgg 240
atatacggtc acacatcaga ggaacagtcg ataccagcta aaggggaata tttcagaagg 300
aaatgtgtcc ttgaccatag agaacactgt tgtgggtgat ggtggtccct attgctgtgt 360
agtggagata cctggagcgt tccattttgt ggactatatg ttggaagtta aaccagaaat 420
ttccacgagt ccaccaacaa ggcccacagc tacaggaaga ccacaaacta tttcaacaag 480
atccacacat gtaccaacat caaccagagt ctctacctct acttctccaa caccagcaca 540
cacagagacc tacaaaccag aggccactac attttatcca gatcagacta cagctgaggt 600
gacagaaacc ttaccctcta ctctgcaga ctggcataac actgtgacat cctcagatga 660
cccttgggat gataacactg aagtaatccc tccacagaag ccacagaaaa acctgaataa 720
gggcttctat gttggcatct ccattgcagc cctgctgata ttgatgcttc tgagcaccat 780
ggttatcacc aggtacgtgg ttatgaaaaa gaagtcagaa tctctgagct tcgttgccct 840
ccctatctct aagattggag cttcccccaa aaaagtgggc gaacggacca gatgtgaaga 900
ccagggtctac attattgaag acactcctta ccccgaagaa gagtccctagt gcctctac 958

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<210> 9
<211> 281
<212> PRT
<213> Mus musculus

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<220>
<221> VARIANT
<222> (1)...(281)
<223> TIM-3 BALB/c allele

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          20          25          30
Asn Ala Tyr Leu Pro Cys Ser Tyr Thr Leu Pro Thr Ser Gly Thr Leu
          35          40          45
Val Pro Met Cys Trp Gly Lys Gly Phe Cys Pro Trp Ser Gln Cys Thr
          50          55          60
Asn Glu Leu Leu Arg Thr Asp Glu Arg Asn Val Thr Tyr Gln Lys Ser
65          70          75          80
Ser Arg Tyr Gln Leu Lys Gly Asp Leu Asn Lys Gly Asp Val Ser Leu
          85          90          95
Ile Ile Lys Asn Val Thr Leu Asp Asp His Gly Thr Tyr Cys Cys Arg
          100         105         110
Ile Gln Phe Pro Gly Leu Met Asn Asp Lys Lys Leu Glu Leu Lys Leu
          115         120         125
Asp Ile Lys Ala Ala Lys Val Thr Pro Ala Gln Thr Ala His Gly Asp
          130         135         140
Ser Thr Thr Ala Ser Pro Arg Thr Leu Thr Thr Glu Arg Asn Gly Ser
145         150         155         160
Glu Thr Gln Thr Leu Val Thr Leu His Asn Asn Asn Gly Thr Lys Ile
          165         170         175
Ser Thr Trp Ala Asp Glu Ile Lys Asp Ser Gly Glu Thr Ile Arg Thr
          180         185         190
Ala Ile His Ile Gly Val Gly Val Ser Ala Gly Leu Thr Leu Ala Leu
          195         200         205
Ile Ile Gly Val Leu Ile Leu Lys Trp Tyr Ser Cys Lys Lys Lys Lys
210         215         220
Leu Ser Ser Leu Ser Leu Ile Thr Leu Ala Asn Leu Pro Pro Gly Gly
225         230         235         240
Leu Ala Asn Ala Gly Ala Val Arg Ile Arg Ser Glu Glu Asn Ile Tyr
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Thr Ile Glu Glu Asn Val Tyr Glu Val Glu Asn Ser Asn Glu Tyr Tyr  
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 Cys Tyr Val Asn Ser Gln Gln Pro Ser  
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<210> 10  
 <211> 2725  
 <212> DNA  
 <213> Mus musculus

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 agttacactc tacctacatc tgggacactt gtgcctatgt gctggggcaa gggattctgt 240  
 ccttggtcac agtgtacca tgaagtgctc agaactgatg aaagaaatgt gacatatcag 300  
 aaatccagca gataccagct aaagggcgat ctcaacaaag gagatgtgtc tctgatcata 360  
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 tgggctgatg aaattaagga ctctggagaa acgatcagaa ctgctatcca cattggagtg 660  
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 tcctgtaaga aaaagaagtt atcgagtttg agccttatta cactggccaa cttgcctcca 780  
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 gaacctgcac acacacacac acacacacac acacacacac acacacacac acacatgaaa 1860  
 tgaagggtct ctctgtgcct gctacctctc tataacatgt atctctacag gactctcctc 1920  
 tgcctctgtt aagacatgag tgggagcatg gcagagcagt ccagtaatta attccagcac 1980  
 tcagaaggct ggagcagaag cgtggagagt tcaggagcac tgtgcccac actgccagac 2040  
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 gcgaaaaggca aactttgact gttgtgtgct caagggggaa tgactcagac aacttctcca 2160  
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 aactgtgtac atcagaggac atctgttagt gaggacacca aaacctgtgg taccgttttt 2520  
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<210> 11  
 <211> 281

<212> PRT  
 <213> Mus musculus

<220>  
 <221> VARIANT  
 <222> (1)...(281)  
 <223> TIM-3, C.D2 ES-HBA and DBA/2J allele

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 20 25 30  
 Asn Ala Tyr Leu Pro Cys Ser Tyr Thr Leu Ser Thr Pro Gly Ala Leu  
 35 40 45  
 Val Pro Met Cys Trp Gly Lys Gly Phe Cys Pro Trp Ser Gln Cys Thr  
 50 55 60  
 Asn Glu Leu Leu Arg Thr Asp Glu Arg Asn Val Thr Tyr Gln Lys Ser  
 65 70 75 80  
 Ser Arg Tyr Gln Leu Lys Gly Asp Leu Asn Lys Gly Asp Val Ser Leu  
 85 90 95  
 Ile Ile Lys Asn Val Thr Leu Asp Asp His Gly Thr Tyr Cys Cys Arg  
 100 105 110  
 Ile Gln Phe Pro Gly Leu Met Asn Asp Lys Lys Leu Glu Leu Lys Leu  
 115 120 125  
 Asp Ile Lys Ala Ala Lys Val Thr Pro Ala Gln Thr Ala His Gly Asp  
 130 135 140  
 Ser Thr Thr Ala Ser Pro Arg Thr Leu Thr Thr Glu Arg Asn Gly Ser  
 145 150 155 160  
 Glu Thr Gln Thr Leu Val Thr Leu His Asn Asn Asn Gly Thr Lys Ile  
 165 170 175  
 Ser Thr Trp Ala Asp Glu Ile Lys Asp Ser Gly Glu Thr Ile Arg Thr  
 180 185 190  
 Ala Ile His Ile Gly Val Gly Val Ser Ala Gly Leu Thr Leu Ala Leu  
 195 200 205  
 Ile Ile Gly Val Leu Ile Leu Lys Trp Tyr Ser Cys Lys Lys Lys Lys  
 210 215 220  
 Leu Ser Ser Leu Ser Leu Ile Thr Leu Ala Asn Leu Pro Pro Gly Gly  
 225 230 235 240  
 Leu Ala Asn Ala Gly Ala Val Arg Ile Arg Ser Glu Glu Asn Ile Tyr  
 245 250 255  
 Thr Ile Glu Glu Asn Val Tyr Glu Val Glu Asn Ser Asn Glu Tyr Tyr  
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 Cys Tyr Val Asn Ser Gln Gln Pro Ser  
 275 280

<210> 12  
 <211> 862  
 <212> DNA  
 <213> Mus musculus

<400> 12  
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 tctgccctgc agttacactc tatctacacc tggggcactt gtgcctatgt gctggggcaa 180  
 gggattctgt ccttggtcac agtgtaccaa cgagttgctc agaactgatg aaagaaatgt 240  
 gacatatcag aaatccagca gataccagct aaagggcgat ctcaacaaag gagacgtgtc 300  
 tctgatcata aagaatgtga ctctggatga ccatgggacc tactgctgca ggatacagtt 360  
 ccctgggtctt atgaatgata aaaaattaga actgaaatta gacatcaaag cagccaaggt 420  
 cactccagct cagactgccc atggggactc tactacagct tctccaagaa ccctaaccac 480



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ggagagaaat ggttcagaga cacagacact ggtgaccctc cataataaca atggaacaaa 540
aatttccaca tgggctgatg aaattaagga ctctggagaa acgatcagaa ctgctatcca 600
cattggagtg ggagtctctg ctgggttgac cctggcactt atcattggtg tcttaatcct 660
taaatggtat tcctgtaaga aaaagaagtt atcgagtttg agccttatta cactggccaa 720
cttgccctca ggaggggttg caaatgcagg agcagtcagg attcgctctg aggaaaatat 780
ctacaccatc gaggagaacg tatatgaagt ggagaattca aatgagtact actgctacgt 840
caacagccag cagccatcct ga 862

```

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<210> 13
<211> 345
<212> PRT
<213> Mus musculus

```

```

<220>
<221> VARIANT
<222> (1)...(345)
<223> TIM-4, BALB/c allele

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<400> 13
Met Ser Lys Gly Leu Leu Leu Trp Leu Val Thr Glu Leu Trp Trp
1 5 10 15
Leu Tyr Leu Ser Lys Ser Pro Ala Ala Ser Glu Asp Thr Ile Ile Gly
20 25 30
Phe Leu Gly Gln Pro Val Thr Leu Pro Cys His Tyr Leu Ser Trp Ser
35 40 45
Gln Ser Arg Asn Ser Met Cys Trp Gly Lys Gly Ser Cys Pro Asn Ser
50 55 60
Lys Cys Asn Ala Glu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser
65 70 75 80
Arg Lys Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu
85 90 95
Val Ser Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr
100 105 110
Cys Cys Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn
115 120 125
Val Arg Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr
130 135 140
Thr Thr Arg Pro Thr Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu
145 150 155 160
Leu Leu Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr
165 170 175
Pro Pro Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr
180 185 190
Cys Pro Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly
195 200 205
Ser Ala Ile Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser
210 215 220
Gln Arg Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro
225 230 235 240
Thr Gly Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr
245 250 255
Gln Lys Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys
260 265 270
Ser His Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys
275 280 285
Val Gly Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Leu Arg
290 295 300
Gly Lys Val Thr Gly Ala Asn Cys Leu Gln Arg His Lys Arg Pro Asp
305 310 315 320
Asn Thr Glu Val Ser Asp Ser Phe Leu Asn Asp Ile Ser His Gly Arg
325 330 335

```

Asp Asp Glu Asp Gly Ile Phe Thr Leu  
340 345

<210> 14  
<211> 1032  
<212> DNA  
<213> Mus musculus

<400> 14  
atgtccaagg ggctttctct cctctggctg gtgacggagc tctgggtggct ttatctgaca 60  
ccagctgcct cagaggatac aataataggg tttttgggcc agccggtgac tttgccttgt 120  
cattacctct cgtgggtcca gagcgcaac agtatgtgct ggggcaaagg ttcattgtccc 180  
aattccaagt gcaatgcaga gcttctccgt acagatggaa caagaatcat ctccaggaag 240  
tcaacaaaat atacactttt ggggaaggtc cagtttggtg aagtgtcctt gaccatctca 300  
aacaccaatc gaggtgacag tggggtgtac tgctgccgta tagaggtgcc tggctggttc 360  
aatgatgtca agaagaatgt gcgcttgagg ctgaggagag ccacaacaac caaaaaacca 420  
acaacaacca cccggccaac caccaccctt tatgtaacca ccaccacccc agagctgctt 480  
ccaacaacag tcatgaccac atctgttctt ccaaccacca caccaccca gacactagcc 540  
accactgcct tcagtacagc agtgaccacg tgccctcaa caacacctgg ctcttctca 600  
caagaaacca caaagggtc cgccatcact acagaatcag aaactctgcc tgcattcaat 660  
cactctcaaa gaagcatgat gaccatatct acagacatag ccgtactcag gccacaggc 720  
tctaaccctg ggattctccc atccacttca cagctgacga cacagaaaac aacattaaca 780  
acaagtgagt ctttgcagaa gacaactaaa tcacatcaga tcaacagcag acagaccatc 840  
ttgatcattg cctgctgtgt gggatttgtg ctaatggtgt tattgtttct ggcgtttctc 900  
cttcgaggga aagtcacagg agccaactgt ttgcagagac acaagaggcc agacaacact 960  
gaagatagtg acagcgtcct caatgacatg tcacacggga gggatgatga agacgggatc 1020  
ttcactctct ga 1032

<210> 15  
<211> 345  
<212> PRT  
<213> Mus musculus

<220>  
<221> VARIANT  
<222> (1)...(345)  
<223> C.D2 ES-HBA and DBA/2J allele

<400> 15  
Met Ser Lys Gly Leu Leu Leu Leu Trp Leu Val Met Glu Leu Trp Trp  
1 5 10 15  
Leu Tyr Leu Ser Lys Ser Pro Ala Ala Ser Glu Asp Thr Ile Ile Gly  
20 25 30  
Phe Leu Gly Gln Pro Val Thr Leu Pro Cys His Tyr Leu Ser Trp Ser  
35 40 45  
Gln Ser Arg Asn Ser Met Cys Trp Gly Lys Gly Ser Cys Pro Asn Ser  
50 55 60  
Lys Cys Asn Ala Glu Leu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser  
65 70 75 80  
Arg Lys Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu  
85 90 95  
Val Ser Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr  
100 105 110  
Cys Cys Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn  
115 120 125  
Val Arg Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr  
130 135 140  
Thr Thr Arg Pro Thr Thr Pro Tyr Val Thr Thr Thr Pro Glu  
145 150 155 160  
Leu Leu Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr Thr

				165					170					175			
Pro	Pro	Gln	Thr	Leu	Ala	Thr	Thr	Ala	Phe	Ser	Thr	Ala	Val	Thr	Thr		
			180					185					190				
Cys	Pro	Ser	Thr	Thr	Pro	Gly	Ser	Phe	Ser	Gln	Glu	Thr	Thr	Lys	Gly		
		195					200					205					
Ser	Ala	Phe	Thr	Thr	Glu	Ser	Glu	Thr	Leu	Pro	Ala	Ser	Asn	His	Ser		
	210					215					220						
Gln	Arg	Ser	Met	Met	Thr	Ile	Ser	Thr	Asp	Ile	Ala	Val	Leu	Arg	Pro		
225					230				235						240		
Thr	Gly	Ser	Asn	Pro	Gly	Ile	Leu	Pro	Ser	Thr	Ser	Gln	Leu	Thr	Thr		
			245					250						255			
Gln	Lys	Thr	Thr	Leu	Thr	Thr	Ser	Glu	Ser	Leu	Gln	Lys	Thr	Thr	Lys		
		260					265					270					
Ser	His	Gln	Ile	Asn	Ser	Arg	Gln	Thr	Ile	Leu	Ile	Ile	Ala	Cys	Cys		
	275						280				285						
Val	Gly	Phe	Val	Leu	Met	Val	Leu	Leu	Phe	Leu	Ala	Phe	Leu	Leu	Arg		
	290				295				300								
Gly	Lys	Val	Thr	Gly	Ala	Asn	Cys	Leu	Gln	Arg	His	Lys	Arg	Pro	Asp		
305					310				315						320		
Asn	Thr	Glu	Val	Ser	Asp	Ser	Phe	Leu	Asn	Asp	Ile	Ser	His	Gly	Arg		
			325					330						335			
Asp	Asp	Glu	Asp	Gly	Ile	Phe	Thr	Leu									
		340					345										

<210> 16  
 <211> 1032  
 <212> DNA  
 <213> Mus musculus

<400> 16  
 atgtccaagg ggctttctcct cctctggctg gtgatggagc tctgggtggct ttatctgaca 60  
 ccagctgcct cagaggatagc aataataggg tttttgggcc agccggtgac tttgccttgt 120  
 cattacctct cgtgggtccca gagccgcaac agtatgtgct ggggcaaagg ttcattgtccc 180  
 aattccaagt gcaatgcaga gcttctccgt acagatggaa caagaatcat ctccaggaag 240  
 tcaacaaaat atacactttt ggggaagggtc cagtttggtg aagtgtcctt gaccatctca 300  
 aacaccaatc gaggtgacag tgggggtgtac tgctgccgta tagaggtgcc tggctgggttc 360  
 aatgatgtca agaagaatgt gcgcttgag ctgaggagag ccacaacaac caaaaaacca 420  
 acaacaacca cccggccaac caccaccct tatgtaacca ccaccacccc agagctgctt 480  
 ccaacaacag tcatgaccac atctgttctt ccaaccacca caccacccc gacactagcc 540  
 accactgcct tcagtacagc agtgaccacg tgcccctcaa caacacctgg ctcttctca 600  
 caagaaacca caaaagggtc cgccttcact acagaatcag aaactctgcc tgcattccat 660  
 cactctcaaa gaagcatgat gaccatatct acagacatag ccgtactcag gccacaggc 720  
 tctaaccctg ggattctccc atccacttca cagctgacga cacagaaaac aacattaaca 780  
 acaagtgagt ctttgcgaga gacaactaaa tcacatcaga tcaacagcag acagaccatc 840  
 ttgatcattg cctgctgtgt gggatttgtg ctaatgggtg tattgtttct ggcgtttctc 900  
 cttcgaggga aagtcacagg agccaactgt ttgcagagac acaagaggcc agacaacact 960  
 gaagatagtg acagcgtcct caatgacatg tcacacggga gggatgatga agacgggatc 1020  
 ttcactctct ga 1032

<210> 17  
 <211> 359  
 <212> PRT  
 <213> H. sapiens

<220>  
 <221> VARIANT  
 <222> (1) ... (360)  
 <223> TIM-1 allele 1

<400> 17

Met	His	Pro	Gln	Val	Val	Ile	Leu	Ser	Leu	Ile	Leu	His	Leu	Ala	Asp
1				5					10					15	
Ser	Val	Ala	Gly	Ser	Val	Lys	Val	Gly	Gly	Glu	Ala	Gly	Pro	Ser	Val
			20					25					30		
Thr	Leu	Pro	Cys	His	Tyr	Ser	Gly	Ala	Val	Thr	Ser	Met	Cys	Trp	Asn
		35					40					45			
Arg	Gly	Ser	Cys	Ser	Leu	Phe	Thr	Cys	Gln	Asn	Gly	Ile	Val	Trp	Thr
	50					55					60				
Asn	Gly	Thr	His	Val	Thr	Tyr	Arg	Lys	Asp	Thr	Arg	Tyr	Lys	Leu	Leu
65					70					75				80	
Gly	Asp	Leu	Ser	Arg	Arg	Asp	Val	Ser	Leu	Thr	Ile	Glu	Asn	Thr	Ala
				85				90						95	
Val	Ser	Asp	Ser	Gly	Val	Tyr	Cys	Cys	Arg	Val	Glu	His	Arg	Gly	Trp
			100					105					110		
Phe	Asn	Asp	Met	Lys	Ile	Thr	Val	Ser	Leu	Glu	Ile	Val	Pro	Pro	Lys
		115					120					125			
Val	Thr	Thr	Thr	Pro	Ile	Val	Thr	Thr	Val	Pro	Thr	Val	Thr	Thr	Val
	130					135					140				
Arg	Thr	Ser	Thr	Thr	Val	Pro	Thr	Thr	Thr	Thr	Val	Pro	Thr	Thr	Thr
145					150					155				160	
Val	Pro	Thr	Thr	Met	Ser	Ile	Pro	Thr	Thr	Thr	Thr	Val	Pro	Thr	Thr
				165					170					175	
Met	Thr	Val	Ser	Thr	Thr	Thr	Ser	Val	Pro	Thr	Thr	Thr	Ser	Ile	Pro
			180					185					190		
Thr	Thr	Thr	Ser	Val	Pro	Val	Thr	Thr	Thr	Val	Ser	Thr	Phe	Val	Pro
		195					200					205			
Pro	Met	Pro	Leu	Pro	Arg	Gln	Asn	His	Glu	Pro	Val	Ala	Thr	Ser	Pro
	210					215					220				
Ser	Ser	Pro	Gln	Pro	Ala	Glu	Thr	His	Pro	Thr	Thr	Leu	Gln	Gly	Ala
225					230					235				240	
Ile	Arg	Arg	Glu	Pro	Thr	Ser	Ser	Pro	Leu	Tyr	Ser	Tyr	Thr	Thr	Asp
				245					250					255	
Gly	Asn	Asp	Thr	Val	Thr	Glu	Ser	Ser	Asp	Gly	Leu	Trp	Asn	Asn	Asn
			260					265					270		
Gln	Thr	Gln	Leu	Phe	Leu	Glu	His	Ser	Leu	Leu	Thr	Ala	Asn	Thr	Thr
		275					280					285			
Lys	Gly	Ile	Tyr	Ala	Gly	Val	Cys	Ile	Ser	Val	Leu	Val	Leu	Leu	Ala
	290					295					300				
Leu	Leu	Gly	Val	Ile	Ile	Ala	Lys	Lys	Tyr	Phe	Phe	Lys	Lys	Glu	Val
305					310					315				320	
Gln	Gln	Leu	Ser	Val	Ser	Phe	Ser	Ser	Leu	Gln	Ile	Lys	Ala	Leu	Gln
				325					330					335	
Asn	Ala	Val	Glu	Lys	Glu	Val	Gln	Ala	Glu	Asp	Asn	Ile	Tyr	Ile	Glu
			340					345					350		
Asn	Ser	Leu	Tyr	Ala	Thr	Asp									
		355													

<210> 18

<211> 1080

<212> DNA

<213> H. sapiens

<400> 18

atgcatacctc	aagtgggtcat	cttaagcctc	atcctacatc	tggcagattc	tgtagctggg	60
tctgtaaaagg	ttgggtggaga	ggcagggtcca	tctgtcacac	taccctgcc	ctacagtgg	120
gctgtcacat	caatgtgctg	gaatagaggc	tcatgttctc	tattcacatg	ccaaaatggc	180
attgtctgga	ccaatggaac	ccacgtcacc	tatcggaagg	acacacgcta	taagctattg	240
ggggaccttt	caagaaggga	tgtctctttg	accatagaaa	atacagctgt	gtctgacagt	300
ggcgtatatt	gttgccgtgt	tgagcaccgt	gggtggttca	atgacatgaa	aatcaccgta	360
tcattggaga	ttgtgccacc	caaggtcacg	actactccaa	ttgtcacaac	tgttccaacc	420

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gtcacgactg ttcgaacgag caccactgtt ccaacgacaa cgactgttcc aacgacaact 480
gttccaacaa caatgagcat tccaacgaca acgactgttc cgacgacaat gactgtttca 540
acgacaacga gcgttccaac gacaacgagc attccaacaa caacaagtgt tccagtgaca 600
acaacgggtct ctacctttgt tcttccaatg cctttgcccc ggcagaacca tgaaccagta 660
gccacttcac catcttcacc tcagccagca gaaacccacc ctacgacact gcagggagca 720
ataaggagag aaccaccag ctcaccattg tactcttaca caacagatgg gaatgacacc 780
gtgacagagt cttcagatgg cctttggaat aacaatcaaa ctcaactgtt cctagaacat 840
agtctactga cggccaatac cactaaagga atctatgctg gagtctgtat ttctgtcttg 900
gtgcttcttg ctcttttggg tgtcatcatt gccaaaaagt atttcttcaa aaaggagggt 960
caacaactaa gtgtttcatt tagcagcctt caaattaaag ctttgcaaaa tgcagttgaa 1020
aaggaagtcc aagcagaaga caatatctac attgagaata gtctttatgc cacggactaa 1080

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<210> 19
<211> 359
<212> PRT
<213> H. sapiens

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<220>
<221> VARIANT
<222> (1)...(359)
<223> TIM-1, allele 2

```

```

<400> 19
Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
 1          5          10          15
Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
          20          25          30
Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn
          35          40          45
Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr
          50          55          60
Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu
          65          70          75          80
Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala
          85          90          95
Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp
          100          105          110
Phe Asn Asp Met Lys Ile Thr Val Ser Leu Glu Ile Val Pro Pro Lys
          115          120          125
Val Thr Thr Thr Pro Ile Val Thr Thr Val Pro Thr Val Thr Thr Val
          130          135          140
Arg Thr Ser Thr Thr Val Pro Thr Thr Thr Thr Val Pro Thr Thr Thr
          145          150          155          160
Val Pro Thr Thr Met Ser Ile Pro Thr Thr Thr Val Pro Thr Thr Thr
          165          170          175
Met Thr Val Ser Thr Thr Thr Ser Val Pro Thr Thr Thr Ser Ile Pro
          180          185          190
Thr Thr Thr Ser Val Pro Val Thr Thr Ala Val Ser Thr Phe Val Pro
          195          200          205
Pro Met Pro Leu Pro Arg Gln Asn His Glu Pro Val Ala Thr Ser Pro
          210          215          220
Ser Ser Pro Gln Pro Ala Glu Thr His Pro Thr Thr Leu Gln Gly Ala
          225          230          235          240
Ile Arg Arg Glu Pro Thr Ser Ser Pro Leu Tyr Ser Tyr Thr Thr Asp
          245          250          255
Gly Asn Asp Thr Val Thr Glu Ser Ser Asp Gly Leu Trp Asn Asn Asn
          260          265          270
Gln Thr Gln Leu Phe Leu Glu His Ser Leu Leu Thr Ala Asn Thr Thr
          275          280          285
Lys Gly Ile Tyr Ala Gly Val Cys Ile Ser Val Leu Val Leu Leu Ala

```

290                      295                      300  
 Leu Leu Gly Val Ile Ile Ala Lys Lys Tyr Phe Phe Lys Lys Glu Val  
 305                      310                      315                      320  
 Gln Gln Leu Ser Val Ser Phe Ser Ser Leu Gln Ile Lys Ala Leu Gln  
                          325                      330                      335  
 Asn Ala Val Glu Lys Glu Val Gln Ala Glu Asp Asn Ile Tyr Ile Glu  
                          340                      345                      350  
 Asn Ser Leu Tyr Ala Thr Asp  
                          355

<210> 20  
 <211> 1080  
 <212> DNA  
 <213> H. sapiens

<400> 20  
 atgcacccctc aagtgggtcat cttaagcctc atcctacatc tggcagattc tgtagctggg 60  
 tctgtaaagg ttggtggaga ggcagggtcca tctgtcacac taccctgcca ctacagtggg 120  
 gctgtcacat caatgtgctg gaatagaggc tcatgttctc tattcacatg ccaaaatggc 180  
 attgtctgga ccaatggaac ccacgtcacc tctcggaagg acacacgcta taagctattg 240  
 ggggaccttt caagaaggga tgtctctttg accatagaaa atacagctgt gtctgacagt 300  
 ggcgtatatatt gttgccgtgt tgagcacctg ggggtggttca atgacatgaa aatcacctga 360  
 tcattggaga ttgtgccacc caaggtcacg actactccaa ttgtcacaac tgttccaacc 420  
 gtacacgactg ttccaacgag caccactgtt ccaacgacaa cgactgttcc aacgacaact 480  
 gttccaacaa caatgagcat tccaacgaca acgactgttc cgacgacaat gactgtttca 540  
 acgacaacga gcgttccaac gacaacgagc attccaacaa caacaagtgt tccagtga 600  
 acagcgggtct ctacctttgt tcctccaatg cctttgcccc ggcagaacca tgaaccagta 660  
 gccacttcac catcttcacc tcagccagca gaaacccacc ctacgacact gcagggagca 720  
 ataaggagag aacccaccag ctcaccattg tactcttaca caacagatgg gaatgacacc 780  
 gtgacagagt cttcagatgg cctttggaat aacaatcaaa ctcaactgtt cctagaacat 840  
 agtctactga cggccaatac cactaaagga atctatgctg gagtctgtat ttctgtcttg 900  
 gtgcttcttg ctcttttggg tgtcatcatt gccaaaaagt atttcttcaa aaaggaggtt 960  
 caacaactaa gtgtttcatt tagcagcctt caaattaaag ctttgcaaaa tgcagttgaa 1020  
 aagggaagtcc aagcagaaga caatatctac attgagaata gtctttatgc cacggactaa 1080

<210> 21  
 <211> 365  
 <212> PRT  
 <213> H. sapiens

<220>  
 <221> VARIANT  
 <222> (1)...(365)  
 <223> TIM-1, allele 3

<400> 21  
 Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp  
 1                      5                      10                      15  
 Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val  
                          20                      25                      30  
 Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn  
                          35                      40                      45  
 Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr  
                          50                      55                      60  
 Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu  
 65                      70                      75                      80  
 Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala  
                          85                      90                      95  
 Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp



<210> 23  
 <211> 359  
 <212> PRT  
 <213> H. sapiens

<220>  
 <221> VARIANT  
 <222> (1)...(359)  
 <223> TIM-1, allele 4

<400> 23  
 Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp  
 1 5 10 15  
 Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val  
 20 25 30  
 Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn  
 35 40 45  
 Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr  
 50 55 60  
 Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu  
 65 70 75 80  
 Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala  
 85 90 95  
 Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp  
 100 105 110  
 Phe Asn Asp Met Lys Ile Thr Val Ser Leu Glu Ile Val Pro Pro Lys  
 115 120 125  
 Val Thr Thr Thr Pro Ile Val Thr Thr Val Pro Thr Val Thr Thr Val  
 130 135 140  
 Arg Thr Ser Thr Thr Val Pro Thr Thr Thr Thr Val Pro Thr Thr Thr  
 145 150 155 160  
 Val Pro Thr Thr Met Ser Ile Pro Thr Thr Thr Thr Val Pro Thr Thr  
 165 170 175  
 Met Thr Val Ser Thr Thr Thr Ser Val Pro Thr Thr Thr Ser Ile Pro  
 180 185 190  
 Thr Thr Thr Ser Val Pro Val Thr Thr Ser Val Ser Thr Phe Val Pro  
 195 200 205  
 Pro Met Pro Leu Pro Arg Gln Asn His Glu Pro Val Ala Thr Ser Pro  
 210 215 220  
 Ser Ser Pro Gln Pro Ala Glu Thr His Pro Thr Thr Leu Gln Gly Thr  
 225 230 235 240  
 Ile Arg Arg Glu Pro Thr Ser Ser Pro Leu Tyr Ser Tyr Thr Thr Asp  
 245 250 255  
 Gly Asn Asp Thr Val Thr Glu Ser Ser Asp Gly Leu Trp Ser Asn Asn  
 260 265 270  
 Gln Thr Gln Leu Phe Leu Glu His Ser Leu Leu Thr Ala Asn Thr Thr  
 275 280 285  
 Lys Gly Ile Tyr Ala Gly Val Cys Ile Ser Val Leu Val Leu Leu Ala  
 290 295 300  
 Leu Leu Gly Val Ile Ile Ala Lys Lys Tyr Phe Phe Lys Lys Glu Val  
 305 310 315 320  
 Gln Gln Leu Ser Val Ser Phe Ser Ser Leu Gln Ile Lys Ala Leu Gln  
 325 330 335  
 Asn Ala Val Glu Lys Glu Val Gln Ala Glu Asp Asn Ile Tyr Ile Glu  
 340 345 350  
 Asn Ser Leu Tyr Ala Thr Asp  
 355

<210> 24  
 <211> 1079



<212> DNA  
 <213> H. sapiens

<400> 24  
 atgcatcctc aagtggatcat ctttaagcctc atcctacatc tggcagattc ttagactggt 60  
 tctgtaaagg ttggtggaga ggcaggtcca tctgtcacac taccctgcca ctacagtgga 120  
 gctgtcacat caatgtgctg gaatagaggc tcatgttctc tattcacatg ccaaaatggc 180  
 attgtctgga ccaatggaac ccacgtcacc tatcggaagg acacacgcta taagctattg 240  
 ggggaccttt caagaaggga tgtctctttg accatagaaa atacagctgt gtctgacagt 300  
 ggcgtatatt gttgccgtgt tgagcaccgt ggggtggttca atgacatgaa aatcaccgta 360  
 tcattggaga ttgtgccacc caagggtcacg actactccaa ttgtcacaac tgttccaacc 420  
 gtcacgactg ttccaacgag caccactgtt ccaacgacaa cgactgttcc aacgacaact 480  
 gttccaacaa caatgagcat tccaacgaca acggactgtt ccgacgacaa tgactgttcc 540  
 aacgacaacg agcgttccaa cgacaacgag cattccaaca acaacaagtg ttccagttag 600  
 aacatgtctc tacctttgtt cctccaatgc ctttgcccag gcagaacctat gaaccagttag 660  
 ccacttcacc atcttcacct cagccagcag aaaccacccc tacgacactg cagggagcaa 720  
 taaggagaga acccaccagc tcaccattgt actcttacac aacagatggg aatgacaccg 780  
 tgacagagtc ttcagatggc ctttggartt acaatcaaac tcaactgttc ctagaacata 840  
 gtctactgac ggccaataacc actaaaggaa tctatgctgg agtctgtatt tctgtcttgg 900  
 tgcttcttgc tcttttgggt gtcattcattg ccaaaaagta tttcttcaaa aaggaggttc 960  
 aacaactaag tgtttcattt agcagccttc aaattaaagc tttgcaaaat gcagttgaaa 1020  
 aggaagtcca agcagaagac aatatctaca ttgagaatag tctttatgcc acggactaa 1079

<210> 25  
 <211> 364  
 <212> PRT  
 <213> H. sapiens

<220>  
 <221> VARIANT  
 <222> (1)... (364)  
 <223> TIM-1 allele 5

<400> 25  
 Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp  
 1 5 10 15  
 Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val  
 20 25 30  
 Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn  
 35 40 45  
 Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr  
 50 55 60  
 Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu  
 65 70 75 80  
 Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala  
 85 90 95  
 Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp  
 100 105 110  
 Phe Asn Asp Met Lys Ile Thr Val Ser Leu Glu Ile Val Pro Pro Lys  
 115 120 125  
 Val Thr Thr Thr Pro Ile Val Thr Thr Val Pro Thr Val Thr Thr Val  
 130 135 140  
 Arg Thr Ser Thr Thr Val Pro Thr Thr Thr Val Pro Met Thr Thr  
 145 150 155 160  
 Thr Val Pro Thr Thr Val Pro Thr Thr Met Ser Ile Pro Thr Thr  
 165 170 175  
 Thr Thr Val Pro Thr Thr Met Thr Val Ser Thr Thr Thr Ser Val Pro  
 180 185 190  
 Thr Thr Thr Ser Ile Pro Thr Thr Ser Val Pro Val Thr Thr Thr Val  
 195 200 205  
 Ser Thr Phe Val Pro Pro Met Pro Leu Pro Arg Gln Asn His Glu Pro

210	215	220
Val Ala Thr Ser Pro Ser Ser Pro Gln Pro Ala Glu Thr His Pro Thr		
225	230	235
Thr Leu Gln Gly Ala Ile Arg Arg Glu Pro Thr Ser Ser Pro Leu Tyr		240
	245	250
Ser Tyr Thr Thr Asp Gly Asn Asp Thr Val Thr Glu Ser Ser Asp Gly		255
	260	265
Leu Trp Asn Asn Asn Gln Thr Gln Leu Phe Leu Glu His Ser Leu Leu		270
	275	280
Thr Ala Asn Thr Thr Lys Gly Ile Tyr Ala Gly Val Cys Ile Ser Val		285
	290	295
Leu Val Leu Leu Ala Leu Leu Gly Val Ile Ile Ala Lys Lys Tyr Phe		300
305	310	315
Phe Lys Lys Glu Val Gln Gln Leu Ser Val Ser Phe Ser Ser Leu Gln		320
	325	330
Ile Lys Ala Leu Gln Asn Ala Val Glu Lys Glu Val Gln Ala Glu Asp		335
	340	345
Asn Ile Tyr Ile Glu Asn Ser Leu Tyr Ala Thr Asp		350
355	360	

<210> 26  
 <211> 1095  
 <212> DNA  
 <213> H. sapiens

<400> 26  
 atgcacccctc aagtgggtcat cttaagcctc atcctacatc tggcagattc tgtagctggt 60  
 tctgtaaaagg ttggtggaga ggcagggtcca tctgtcacac taccctgcca ctacagtgga 120  
 gctgtcacat caatgtgctg gaatagaggc tcatgttctc tattcacatg ccaaaatggc 180  
 attgtctgga ccaatggaac ccacgtcacc tatcggaagg acacacgcta taagctattg 240  
 ggggaccttt caagaaggga tgtctctttg accatagaaa atacagctgt gtctgacagt 300  
 ggcgtatatt gttgccgtgt tgagcacctg ggggtggttca atgacatgaa aatcaccgta 360  
 tcattggaga ttgtgccacc caagggtcacg actactccaa ttgtcacaac tgttccaacc 420  
 gtcacgactg ttcgaacgag caccactgtt ccaacgacaa cgactgttcc aatgacaacg 480  
 actgttccaa cgacaactgt tccaacaaca atgagcattc caacgacaac gactgttccg 540  
 acgacaatga ctgtttcaac gacaacgagc gttccaacga caacgagcat tccaacaaca 600  
 agtgttccag tgacaacaac ggtctctacc tttgttcttc caatgccttt gccaggcag 660  
 aaccatgaac cagtagccac ttcacatct tcacctcagc cagcagaaac ccaccctacg 720  
 acactgcagg gagcaataag gagagaaccc accagctcac cattgtactc ttacacaaca 780  
 gatgggaatg acaccgtgac agagtcttca gatggccttt ggaataacaa tcaaaactcaa 840  
 ctgttctctag aacatagtct actgacggcc aataccacta aaggaatcta tgctggagtc 900  
 tgtatttctg tcttggtgct tcttgctctt ttgggtgtca tcattgccaa aaagtatttc 960  
 ttcaaaaagg aggttcaaca actaagtgtt tcatttagca gccttcaa ataaagctttg 1020  
 caaaatgcag ttgaaaagga agtccaagca gaagacaata tctacattga gaatagtctt 1080  
 tatgccacgg actaa 1095

<210> 27  
 <211> 364  
 <212> PRT  
 <213> H. sapiens

<220>  
 <221> VARIANT  
 <222> (1)...(364)  
 <223> TIM-1, allele 6

<400> 27  
 Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp  
 1 5 10 15  
 Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val



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aacaagtgtt ccagtgacaa caacggtctc tacctttgtt cctccaatgc ctttgcccag 660
gcagaacccat gaaccagtag ccacttcacc atcttcacct cagccagcag aaaccacccc 720
tacgacactg cagggagcaa taaggagaga acccaccagc tcaccattgt actcttacac 780
aacagatggg gatgacaccg tgacagagtc ttcagatggc ctttggaata acaatcaaac 840
tcaactgttc ctagaacata gtctactgac ggccaatacc actaaaggaa tctatgctgg 900
agtctgtatt tctgtcttgg tgcttcttgc tcttttgggt gtcattcattg ccaaaaagta 960
tttcttcaaa aaggagggtc aacaactaag tgtttcattt agcagccttc aaattaaagc 1020
tttgcaaaat gcagttgaaa aggaagtcca agcagaagac aatatctaca ttgagaatag 1080
tctttatgcc acggactaa                                     1099

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<210> 29
<211> 301
<212> PRT
<213> H. sapiens

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<220>
<221> VARIANT
<222> (1)...(301)
<223> TIM-3, allele 1

```

```

<400> 29
Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu
1          5          10          15
Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln
20          25          30
Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
35          40          45
Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
50          55          60
Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
65          70          75          80
Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
85          90          95
Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
100         105         110
Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val
115         120         125
Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Arg Gln Arg Asp Phe
130         135         140
Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala
145         150         155         160
Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile
165         170         175
Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu
180         185         190
Arg Asp Ser Gly Ala Thr Ile Arg Ile Gly Ile Tyr Ile Gly Ala Gly
195         200         205
Ile Cys Ala Gly Leu Ala Leu Ala Leu Ile Phe Gly Ala Leu Ile Phe
210         215         220
Lys Trp Tyr Ser His Ser Lys Glu Lys Ile Gln Asn Leu Ser Leu Ile
225         230         235         240
Ser Leu Ala Asn Leu Pro Pro Ser Gly Leu Ala Asn Ala Val Ala Glu
245         250         255
Gly Ile Arg Ser Glu Glu Asn Ile Tyr Thr Ile Glu Glu Asn Val Tyr
260         265         270
Glu Val Glu Glu Pro Asn Glu Tyr Tyr Cys Tyr Val Ser Ser Arg Gln
275         280         285
Gln Pro Ser Gln Pro Leu Gly Cys Arg Phe Ala Met Pro
290         295         300

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<210> 30  
 <211> 1116  
 <212> DNA  
 <213> H. sapiens

<400> 30  
 ggagaggttaa aactgtgcct aacagaggtg tcctctgact tttcttctgc aagctccatg 60  
 ttttcacatc ttccctttga ctgtgtcctg ctgctgctgc tgctactact tacaagggtcc 120  
 tcagaagtgg aatacagagc ggaggtcggg cagaatgcct atctgccctg cttctacacc 180  
 ccagccgccc cagggaaacct cgtgccgctc tgctggggca aaggagcctg tcctgtgttt 240  
 gaatgtggca acgtgggtgct caggactgat gaaagggatg tgaattattg gacatccaga 300  
 tactggctaa atggggattt ccgcaaagga gatgtgtccc tgaccataga gaatgtgact 360  
 ctagcagaca gtgggatcta ctgctgccgg atccaaatcc caggcataat gaatgatgaa 420  
 aaattttaacc tgaagttggg catcaaacca gccaaaggta cccctgcacc gactctgcag 480  
 agagacttca ctgcagcctt tccaaggatg cttaccacca ggggacatgg cccagcagag 540  
 acacagacac tggggagcct ccctgatata aatctaacac aaatatccac attggccaat 600  
 gagttacggg actctagatt ggccaatgac ttacggggact ctggagcaac catcagaata 660  
 ggcattctaca tcggagcagg gatctgtgct gggctggctc tggctcttat cttcggcgct 720  
 ttaattttca aatgggtattc tcatagcaaa gagaagatac agaatttaag cctcatctct 780  
 ttggccaacc tccctccctc aggattggca aatgcagtag cagaggggaat tcgctcagaa 840  
 gaaaacatct ataccattga agagaacgta tatgaagtgg aggagcccaa tgagtattat 900  
 tgctatgtca gcagcaggca gcaaccttca caacctttgg gttgtcgctt tgcaatgccca 960  
 tagatccaac caccttattt ttgagcttgg tgttttgtct ttttcagaaa ctatgagctg 1020  
 tgtcacctga ctgggttttg aggttctgtc cactgctatg gagcagagtt ttcccatatt 1080  
 cagaagataa tgactcacat gggaattgaa ctggga 1116

<210> 31  
 <211> 301  
 <212> PRT  
 <213> H. sapiens

<220>  
 <221> VARIANT  
 <222> (1)...(301)  
 <223> TIM-3, allele 2

<400> 31  
 Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu  
 1 5 10 15  
 Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln  
 20 25 30  
 Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu  
 35 40 45  
 Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly  
 50 55 60  
 Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser  
 65 70 75 80  
 Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr  
 85 90 95  
 Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile  
 100 105 110  
 Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val  
 115 120 125  
 Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Leu Gln Arg Asp Phe  
 130 135 140  
 Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala  
 145 150 155 160  
 Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile  
 165 170 175  
 Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu  
 180 185 190

Arg	Asp	Ser	Gly	Ala	Thr	Ile	Arg	Ile	Gly	Ile	Tyr	Ile	Gly	Ala	Gly
		195					200					205			
Ile	Cys	Ala	Gly	Leu	Ala	Leu	Ala	Leu	Ile	Phe	Gly	Ala	Leu	Ile	Phe
	210					215					220				
Lys	Trp	Tyr	Ser	His	Ser	Lys	Glu	Lys	Ile	Gln	Asn	Leu	Ser	Leu	Ile
225					230					235					240
Ser	Leu	Ala	Asn	Leu	Pro	Pro	Ser	Gly	Leu	Ala	Asn	Ala	Val	Ala	Glu
			245						250					255	
Gly	Ile	Arg	Ser	Glu	Glu	Asn	Ile	Tyr	Thr	Ile	Glu	Glu	Asn	Val	Tyr
			260					265					270		
Glu	Val	Glu	Glu	Pro	Asn	Glu	Tyr	Tyr	Cys	Tyr	Val	Ser	Ser	Arg	Gln
		275					280					285			
Gln	Pro	Ser	Gln	Pro	Leu	Gly	Cys	Arg	Phe	Ala	Met	Pro			
	290					295					300				

<210> 32  
 <211> 1116  
 <212> DNA  
 <213> H. sapiens

<400> 32  
 ggagagttaa aactgtgcct aacagaggtg tcctctgact tttcttctgc aagctccatg 60  
 ttttcacatc ttccctttga ctgtgtcctg ctgctgctgc tgctactact tacaagggtcc 120  
 tcagaagtgg aatacagagc ggaggtcggg cagaatgcct atctgccctg cttctacacc 180  
 ccagccgccc cagggaaacct cgtgcccgtc tgctggggca aaggagcctg tcctgtgttt 240  
 gaatgtggca acgtgggtgct caggactgat gaaagggatg tgaattattg gacatccaga 300  
 tactggctaa atggggattt ccgcaaagga gatgtgtccc tgaccataga gaatgtgact 360  
 ctagcagaca gtgggatcta ctgctgccgg atccaaatcc caggcataat gaatgatgaa 420  
 aaatttaacc tgaagttggg catcaaacca gccaaaggtca cccctgcacc gactcggcag 480  
 agagacttca ctgcagcctt tccaaggatg cttaccacca ggggacatgg cccagcagag 540  
 acacagacac tggggagcct ccctgatata aatctaacac aaatatccac attggccaat 600  
 gagttacggg actctagatt ggccaatgac ttacgggact ctggagcaac catcagaata 660  
 ggcactctaca tcggagcagg gatctgtgct gggtctggctc tggctcttat cttcggcgct 720  
 ttaattttca aatggtattc tcatagcaaa gagaagatac agaatttaag cctcatctct 780  
 ttggccaacc tccctccctc aggattggca aatgcagtag cagaggggaat tcgctcagaa 840  
 gaaaacatct ataccattga agagaacgta tatgaagtgg aggagcccaa tgagtattat 900  
 tgctatgtca gcagcaggca gcaaccctca caacctttgg gttgtcgctt tgcaatgcc 960  
 tagatccaac caccttattt ttgagcttgg tgttttgtct ttttcagaaa ctatgagctg 1020  
 tgtcacctga ctggttttgg aggttctgtc cactgctatg gagcagagtt ttcccatatt 1080  
 cagaagataa tgactcacat gggaattgaa ctggga 1116

<210> 33  
 <211> 378  
 <212> PRT  
 <213> H. sapiens

<220>  
 <221> VARIANT  
 <222> (1)...(378)  
 <223> TIM-4, allele 1

Met	Ser	Lys	Glu	Pro	Leu	Ile	Leu	Trp	Leu	Met	Ile	Glu	Phe	Trp	Trp
1				5					10					15	
Leu	Tyr	Leu	Thr	Pro	Val	Thr	Ser	Glu	Thr	Val	Val	Thr	Glu	Val	Leu
			20					25					30		
Gly	His	Arg	Val	Thr	Leu	Pro	Cys	Leu	Tyr	Ser	Ser	Trp	Ser	His	Asn
		35					40					45			
Ser	Asn	Ser	Met	Cys	Trp	Gly	Lys	Asp	Gln	Cys	Pro	Tyr	Ser	Gly	Cys
	50					55					60				

Lys	Glu	Ala	Leu	Ile	Arg	Thr	Asp	Gly	Met	Arg	Val	Thr	Ser	Arg	Lys
65					70					75					80
Ser	Ala	Lys	Tyr	Arg	Leu	Gln	Gly	Thr	Ile	Pro	Arg	Gly	Asp	Val	Ser
				85					90					95	
Leu	Thr	Ile	Leu	Asn	Pro	Ser	Glu	Ser	Asp	Ser	Gly	Val	Tyr	Cys	Cys
			100					105					110		
Arg	Ile	Glu	Val	Pro	Gly	Trp	Phe	Asn	Asp	Val	Lys	Ile	Asn	Val	Arg
		115					120					125			
Leu	Asn	Leu	Gln	Arg	Ala	Ser	Thr	Thr	Thr	His	Arg	Thr	Ala	Thr	Thr
	130					135					140				
Thr	Thr	Arg	Arg	Thr	Thr	Thr	Thr	Ser	Pro	Thr	Thr	Thr	Arg	Gln	Met
145					150					155					160
Thr	Thr	Thr	Pro	Ala	Ala	Leu	Pro	Thr	Thr	Val	Val	Thr	Thr	Pro	Asp
			165						170					175	
Leu	Thr	Thr	Gly	Thr	Pro	Leu	Gln	Met	Thr	Thr	Ile	Ala	Val	Phe	Thr
			180					185					190		
Thr	Ala	Asn	Thr	Cys	Leu	Ser	Leu	Thr	Pro	Ser	Thr	Leu	Pro	Glu	Glu
	195						200					205			
Ala	Thr	Gly	Leu	Leu	Thr	Pro	Glu	Pro	Ser	Lys	Glu	Gly	Pro	Ile	Leu
	210					215					220				
Thr	Ala	Glu	Ser	Glu	Thr	Val	Leu	Pro	Ser	Asp	Ser	Trp	Ser	Ser	Ala
225					230					235					240
Glu	Ser	Thr	Ser	Ala	Asp	Thr	Val	Leu	Leu	Thr	Ser	Lys	Glu	Ser	Lys
			245					250						255	
Val	Trp	Asp	Leu	Pro	Ser	Thr	Ser	His	Val	Ser	Met	Trp	Lys	Thr	Ser
	260							265					270		
Asp	Ser	Val	Ser	Ser	Pro	Gln	Pro	Gly	Ala	Ser	Asp	Thr	Ala	Val	Pro
	275						280					285			
Glu	Gln	Asn	Lys	Thr	Thr	Lys	Thr	Gly	Gln	Met	Asp	Gly	Ile	Pro	Met
	290					295					300				
Ser	Met	Lys	Asn	Glu	Met	Pro	Ile	Ser	Gln	Leu	Leu	Met	Ile	Ile	Ala
305					310					315					320
Pro	Ser	Leu	Gly	Phe	Val	Leu	Phe	Ala	Leu	Phe	Val	Ala	Phe	Leu	Leu
			325					330						335	
Arg	Gly	Lys	Leu	Met	Glu	Thr	Tyr	Cys	Ser	Gln	Lys	His	Thr	Arg	Leu
			340					345					350		
Asp	Tyr	Ile	Gly	Asp	Ser	Lys	Asn	Val	Leu	Asn	Asp	Val	Gln	His	Gly
	355						360					365			
Arg	Glu	Asp	Glu	Asp	Gly	Leu	Phe	Thr	Leu						
	370					375									

<210> 34  
 <211> 1156  
 <212> DNA  
 <213> H. sapiens

<400> 34  
 atgtccaaag aacctctcat tctctggctg atgattgagt tttggtggct ttacctgaca 60  
 ccagtcactt cagagactgt tgtgacggag gttttgggtc accgggtgac tttgccctgt 120  
 ctgtactcat cctgggtctca caacagcaac agcatgtgct gggggaaaga ccagtgcccc 180  
 tactccgggt gcaaggaggc gtcacccgc actgatggaa tgagggtgac ctcaagaaag 240  
 tcagcaaaat atagacttca ggggactatc ccgagagggt atgtctcctt gaccatctta 300  
 aaccccagtg aaagtgcag cggtgtgtac tgctgccgca tagaagtgcc tggctgggtc 360  
 aacgatgtaa agataaacgt gcgcctgaat ctacagagag cctcaacaac cagcacaga 420  
 acagcaacca ccaccacacg cagaacaaca acaacaagcc ccaccaccac ccgacaaatg 480  
 acaacaacc cagctgcact tccaacaaca gtcgtgacca caccgatct cacaaccgga 540  
 acaccactcc agatgacaac cattgccgtc ttcacaacag caaacacgtg cctttcacta 600  
 accccaagca cccttcggga ggaagccaca ggtcttctga ctcccgagcc ttctaaggaa 660  
 gggcccatcc tctactgcaga atcagaaact gtccctccca gtgattcctg gagtagtgct 720  
 gagtctactt ctgctgacac tgcctgctg acatccaaag agtccaaagt ttgggatctc 780

```

ccatcaacat cccacgtgtc aatgtggaaa acgagtgatt ctgtgtcttc tcctcagcct 840
ggagcatctg atacagcagt tcctgagcag aacaaaacaa caaaaacagg acagatggat 900
ggaataccca tgtcaatgaa gaatgaaatg cccatctccc aactactgat gatcatcgcc 960
ccctccttgg gatttgtgct cttcgcattg tttgtggcgt ttctcctgag agggaaactc 1020
atggaaacct attgttcgca gaaacacaca aggctagact acattggaga tagtaaaaat 1080
gtcctcaatg acgtgcagca tggaagggaa gacgaagacg gcctttttac cctctaacaa 1140
cgcagtagca tggttag                                     1156

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<210> 35
<211> 378
<212> PRT
<213> H. sapiens

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<220>
<221> VARIANT
<222> (1)...(378)
<223> TIM-4, allele 2

```

```

<400> 35
Met Ser Lys Glu Pro Leu Ile Leu Trp Leu Met Ile Glu Phe Trp Trp
 1      5      10      15
Leu Tyr Leu Thr Pro Val Thr Ser Glu Thr Val Val Thr Glu Val Leu
 20      25      30
Gly His Arg Val Thr Leu Pro Cys Leu Tyr Ser Ser Trp Ser His Asn
 35      40      45
Ser Asn Ser Met Cys Trp Gly Lys Asp Gln Cys Pro Tyr Ser Gly Cys
 50      55      60
Lys Glu Ala Leu Ile Arg Thr Asp Gly Met Arg Val Thr Ser Arg Lys
 65      70      75      80
Ser Ala Lys Tyr Arg Leu Gln Gly Thr Ile Pro Arg Gly Asp Val Ser
 85      90      95
Leu Thr Ile Leu Asn Pro Ser Glu Ser Asp Ser Gly Val Tyr Cys Cys
100      105      110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Ile Asn Val Arg
115      120      125
Leu Asn Leu Gln Arg Ala Ser Thr Thr Thr His Arg Thr Ala Thr Thr
130      135      140
Thr Thr Arg Arg Thr Thr Thr Ser Pro Thr Thr Thr Arg Gln Met
145      150      155      160
Thr Thr Thr Pro Ala Leu Pro Thr Thr Val Val Thr Thr Pro Asp
165      170      175
Leu Thr Thr Gly Thr Pro Leu Gln Met Thr Thr Ile Ala Val Phe Thr
180      185      190
Thr Ala Asn Thr Cys Leu Ser Leu Thr Pro Ser Thr Leu Pro Glu Glu
195      200      205
Ala Thr Gly Leu Leu Thr Pro Glu Pro Ser Lys Glu Gly Pro Ile Leu
210      215      220
Thr Ala Glu Ser Glu Thr Val Leu Pro Ser Asp Ser Trp Ser Ser Val
225      230      235      240
Glu Ser Thr Ser Ala Asp Thr Val Leu Leu Thr Ser Lys Glu Ser Lys
245      250      255
Val Trp Asp Leu Pro Ser Thr Ser His Val Ser Met Trp Lys Thr Ser
260      265      270
Asp Ser Val Ser Ser Pro Gln Pro Gly Ala Ser Asp Thr Ala Val Pro
275      280      285
Glu Gln Asn Lys Thr Thr Lys Thr Gly Gln Met Asp Gly Ile Pro Met
290      295      300
Ser Met Lys Asn Glu Met Pro Ile Ser Gln Leu Leu Met Ile Ile Ala
305      310      315      320
Pro Ser Leu Gly Phe Val Leu Phe Ala Leu Phe Val Ala Phe Leu Leu
325      330      335

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Arg Gly Lys Leu Met Glu Thr Tyr Cys Ser Gln Lys His Thr Arg Leu  
                   340                                  345                                  350  
 Asp Tyr Ile Gly Asp Ser Lys Asn Val Leu Asn Asp Val Gln His Gly  
                   355                                  360                                  365  
 Arg Glu Asp Glu Asp Gly Leu Phe Thr Leu  
                   370                                  375

<210> 36  
 <211> 1156  
 <212> DNA  
 <213> H. sapiens

<400> 36  
 atgtccaaag aacctctcat tctctggctg atgattgagt tttgggtggct ttacctgaca 60  
 ccagtcactt cagagactgt tgtgacggag gttttgggtc accgggtgac tttgccctgt 120  
 ctgtactcat cctggtctca caacagcaac agcatgtgct gggggaaaga ccagtgtccc 180  
 tactccggtt gcaaggaggc gctcatccgc actgatggaa tgagggtgac ctcaagaaag 240  
 tcagcaaaat atagacttca ggggactatc ccgagagggtg atgtctcctt gaccatctta 300  
 aaccccagtg aaagtgcagc cgggtgtgtac tgctgccgca tagaagtgcc tggctgggtc 360  
 aacgatgtaa agataaacgt ggcctgaat ctacagagag cctcaacaac cagcacaga 420  
 acagcaacca ccaccacacg cagaacaaca acaacaagcc ccaccaccac ccgacaaatg 480  
 acaacaaccc cagctgcact tccaacaaca gtcgtgacca caccgatct cacaaccgga 540  
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 <213> H. sapiens

<220>  
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 <223> Exon 3, reference sequence

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 tgctcactct catgttgatt tctgactcca gccaaaggta cgactactcc aattgtcaca 180  
 actgttccaa ccgtcacgac tgttcgaacg agcaccactg ttccaacgac aacgactgtt 240  
 ccaacgacaa ctgttccaac aacaatgagc attccaacga caacgactgt tctgacgaca 300  
 atgactgttt caacgacaac gagcgttcca acgacaacga gcattccaac aacaacaagt 360  
 gttccagtga caacaactgt ctctaccttt gttcctccaa tgcccttgcc caggcagaac 420  
 catgaaccag gtaaaacaga tgtgtttgga agcccaaagg ccttctaata aggagctgag 480  
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<210> 38  
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 <212> DNA  
 <213> H. sapiens

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<220>
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<222> (152)...(448)
<223> Exon 3, INS157 polymorphism

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tgctcactct catgttgatt tctgactcca gccaaaggta cgactactcc aattgtcaca      180
actgttccaa ccgtcacgac tggtcgaacg agcaccactg ttccaacgac aacgactggt      240
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acgactgttc tgacgacaat gactgtttca acgacaacga gcgttccaac gacaacgagc      360
attccaacaa caacaagtgt tccagtgaca acaactgtct ctacctttgt tcctccaatg      420
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<220>
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tgctcactct catgttgatt tctgactcca gccaaaggta cgactactcc aattgtcaca      180
actgttccaa ccgtcacgac tggtcgaacg agcaccactg ttccaacgac aacgactggt      240
ccaatgacaa cgactgttcc aacgacaact gttccaacaa caatgagcat tccaacgaca      300
acgactgttc tgacgacaat gactgtttca acgacaacga gcgttccaac gacaacgagc      360
attccaacaa caagtgttcc agtgacaaca actgtctcta cctttgttcc tccaatgcct      420
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<212> DNA
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<220>
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<223> Exon 3, 157insMTVP polymorphism

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tgctcactct catgttgatt tctgactcca gccaaaggta cgactactcc aattgtcaca      180
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actgttctga cgacaatgac tgtttcaacg acaacgagcg ttccaacgac aacgagcatt      360
ccaacaacaa caagtgttcc agtgacaaca actgtctcta cctttgttcc tccaatgcct      420
ttgcccaggc agaaccatga accaggtaaa acagatgtgt ttggaagccc aaaggccttc      480
taatgaggag ctgcgg                                     496

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